IN THE CLAIMS:

Claims 1-48 were previously cancelled. Claim 49 is herein cancelled. Claims 50-54 have been amended herein. New claims 55-58 are presented herein. All of the pending claims are presented below. This listing of claims will replace all prior versions and listings of claims in the application. Please enter these claims as amended.

Listing of the Claims:

1.-49. (Cancelled).

50. (Currently amended) The method according to ~~claim 49~~ claim 52, wherein determining the level of expression is performed with a gene chip.

51. (Currently amended) The method according to ~~claim 49~~ claim 52, wherein the level of expression of each of at least eight cluster-specific genes from cluster #9 is determined.

52. (Currently amended) ~~The~~ A method ~~according to claim 49, wherein the at least five cluster-specific genes from a single cluster are~~ for determining the prognosis for an AML-affected subject, said method comprising the steps of:
determining, in a sample obtained from the subject, a level of expression of each of at least
　　MYH11, CLIPR-59, ST18, NRP1 and CLECSF13 from cluster #9, corresponding to the
　　AML class of inv(16);
establishing the similarity of expression levels between the at least MYH11, CLIPR-59, ST18,
　　NRP1 and CLECSF13 in the AML-affected subject and the at least MYH11, CLIPR-59,
　　ST18, NRP1 and CLECSF13 in subjects selected from the inv(16) class; and
assigning to the AML-affected subject a prognosis based on the established similarity of
　　expression levels between the at least MYH11, CLIPR-59, ST18, NRP1 and CLECSF13
　　in the AML-affected subject and the at least MYH11, CLIPR-59, ST18, NRP1 and
　　CLECSF13 in subjects selected from the inv(16) class.

53.   (Currently amended) ~~The~~ A method ~~according to claim 49, wherein the at least five cluster-specific genes from a single cluster are~~ for determining the prognosis for an AML-affected subject, said method comprising the steps of:

determining, in a sample obtained from the subject, a level of expression of each of at least HGF, FGF13, MEG3, GABRE and MST1 from cluster #12, corresponding to the AML class of t(15; 17);

establishing the similarity of expression levels between the at least FGF13, MEG3, GABRE and MST1 in the AML-affected subject and the at least FGF13, MEG3, GABRE and MST1 in subjects selected from the t(15; 17) class; and

assigning to the AML-affected subject a prognosis based on the established similarity of expression levels between the at least FGF13, MEG3, GABRE and MST1 in the AML-affected subject and the at least FGF13, MEG3, GABRE and MST1 in subjects selected from the t(15; 17) class.

54.   (Currently amended) ~~The~~ A method ~~according to claim 49, wherein the at least five cluster-specific genes from a single cluster are~~ for determining the prognosis for an AML-affected subject, said method comprising the steps of:

determining, in a sample obtained from the subject, a level of expression of each of at least CBFA2T1, ROBO1, CACNA2D2, POU4F1 and IL5RA from cluster #13, corresponding to the AML class of t(8;21);

establishing the similarity of expression levels between the at least CBFA2T1, ROBO1, CACNA2D2, POU4F1 and IL5RA in the AML-affected subject and the at least CBFA2T1, ROBO1, CACNA2D2, POU4F1 and IL5RA in subjects selected from the t(8;21) class; and

assigning to the AML-affected subject a prognosis based on the established similarity of expression levels between the at least CBFA2T1, ROBO1, CACNA2D2, POU4F1 and IL5RA in the AML-affected subject and the at least CBFA2T1, ROBO1, CACNA2D2, POU4F1 and IL5RA in subjects selected from the t(8;21) class.

55.   (New) The method according to claim 53, wherein determining the level of expression is performed with a gene chip.

56.   (New) The method according to claim 53, wherein the level of expression of each of at least eight cluster-specific genes from cluster #12 is determined.

57.   (New) The method according to claim 54, wherein determining the level of expression is performed with a gene chip.

58.   (New) The method according to claim 54, wherein the level of expression of each of at least eight cluster-specific genes from cluster #13 is determined.